

Figure 1: 161P2F10B SSH sequence of 182 nucleotides (SEQ. ID. No. 742)

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1 GATCACACAT TAGGTTATNG ACTTCAATAT TTTCAAATGG TTCAACTTCA GTCTTCTCTT
61 TAAAACTGGG TCCATGTGCC AAGAAAGATA GCCTCCATGC TCCTAAACTC ATTGTTATAA
121 CCATGGTTGC CTCCTCCACA ATTTGTATTT GATTTACTCC TAACAGCCAG CCACTGTTGA
181 TC
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Figure 2.

Figure 2A. The cDNA (SEQ ID. NO. : 744) and amino acid sequence (SEQ ID. NO. : 743) of 161P2F10B. The 3858 nucleotide sequence of 161P2F10B is shown. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 44-2671 including the stop codon.

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1                                     M E S T L T
1 ctactttattctgataaaacaggtctatgcagctaccaggacaATGGAATCTACGTTGAC
7  L A T E Q P V K K N T L K K Y K I A C I
61 TTTAGCAACGGAACAACCTGTTAAGAAGAACACTCTTAAGAAATATAAAATAGCTTGCAT
27  V L L A L L V I M S L G L G L G L G L R
121 TGTTCTTCTTGCTTTGCTGGTGATCATGTCACTTGGATTAGGCCTGGGGCTTGGACTCAG
47  K L E K Q G S C R K K C F D A S F R G L
181 GAAACTGGAAGCAAGGCAGCTGCAGGAAGAAGTGCTTTGATGCATCATTTAGAGGACT
67  E N C R C D V A C K D R G D C C W D F E
241 GGAGAACTGCCGGTGTGATGTGGCATGTAAAGACCGAGGTGATTGCTGCTGGGATTTTGA
87  D T C V E S T R I W M C N K F R C G E T
301 AGACACCTGTGTGGAATCAACTCGAATATGGATGTGCAATAAATTCGTTGTGGAGAGAC
107 R L E A S L C S C S D D C L Q K K D C C
361 CAGATTAGAGGCCAGCCTTTGCTCTTGTTTCAGATGACTGTTTGCAGAAGAAAGATTGCTG
127 A D Y K S V C Q G E T S W L E E N C D T
421 TGCTGACTATAAGAGTGTTCCTGCAAGGAGAAACCTCATGGCTGGAAGAAAACCTGTGACAC
147 A Q Q S Q C P E G F D L P P V I L F S M
481 AGCCCAGCAGTCTCAGTGCCCGAAGGGTTTGACCTGCCACCAGTTATCTTGTTTTCTAT
167 D G F R A E Y L Y T W D T L M P N I N K
541 GGATGGATTTAGAGCTGAATATTTATACACATGGGATACTTTAATGCCAAATATCAATAA
187 L K T C G I H S K Y M R A M Y P T K T F
601 ACTGAAAACATGTGGAATTCATTCAAATACATGAGAGCTATGTATCCTACCAAAACCTT
207 P N H Y T I V T G L Y P E S H G I I D N
661 CCCAAATCATTACACCATTGTACACGGGCTTGTATCCAGAGTCACATGGCATCATTGACAA
227 N M Y D V N L N K N F S L S S K E Q N N
721 TAATATGTATGATGTAAATCTCAACAAGAATTTTCACTTTCTTCAAAGGAACAAAATAA
247 P A W W H G Q P M W L T A M Y Q G L K A
781 TCCAGCCTGGTGGCATGGGCAACCAATGTGGCTGACAGCAATGTATCAAGGTTTAAAGC
267 A T Y F W P G S E V A I N G S F P S I Y
841 CGCTACCTACTTTTGGCCCGGATCAGAAGTGGCTATAAATGGCTCCTTTTCCTTCATATA
287 M P Y N G S V P F E E R I S T L L K W L
901 CATGCCTTACAACGGAAGTGTCCCATTTGAAGAGAGGATTTCTACACTGTTAAAATGGCT
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307 D L P K A E R P R F Y T M Y F E E P D S
 961 GGACCTGCCCCAAGCTGAAAGACCCAGGTTTTATACCATGTATTTTGAAGAACCTGATTC
 327 S G H A G G P V S A R V I K A L Q V V D
 1021 CTCTGGACATGCAGGTGGACCAGTCAGTGCCAGAGTAATTAAAGCCTTACAGGTAGTAGA
 347 H A F G M L M E G L K Q R N L H N C V N
 1081 TCATGCTTTTGGGATGTTGATGGAAGGCCTGAAGCAGCGGAATTTGCACAACCTGTGTCAA
 367 I I L L A D H G M D Q T Y C N K M E Y M
 1141 TATCATCCTTCTGGCTGACCATGGAATGGACCAGACTTATTGTAACAAGATGGAATACAT
 387 T D Y F P R I N F F Y M Y E G P A P R I
 1201 GACTGATTATTTTCCCAGAATAAACTTCTTCTACATGTACGAAGGGCCTGCCCCCGCAT
 407 R A H N I P H D F F S F N S E E I V R N
 1261 CCGAGCTCATAATATACCTCATGACTTTTTTAGTTTTAATTCTGAGGAAATTGTTAGAAA
 427 L S C R K P D Q H F K P Y L T P D L P K
 1321 CCTCAGTTGCCGAAAACCTGATCAGCATTTCAGCCCTATTTGACTCCTGATTTGCCAAA
 447 R L H Y A K N V R I D K V H L F V D Q Q
 1381 GCGACTGCACTATGCCAAGAACGTGAGAATCGACAAAGTTCATCTCTTTGTGGATCAACA
 467 W L A V R S K S N T N C G G G N H G Y N
 1441 GTGGCTGGCTGTTAGGAGTAAATCAAATACAAATTGTGGAGGAGGCAACCATGGTTATAA
 487 N E F R S M E A I F L A H G P S F K E K
 1501 CAATGAGTTTAGGAGCATGGAGGCTATCTTTCTGGCACATGGACCCAGTTTTAAAGAGAA
 507 T E V E P F E N I E V Y N L M C D L L R
 1561 GACTGAAGTTGAACCATTTGAAAATATTGAAGTCTATAACCTAATGTGTGATCTTCTACG
 527 I Q P A P N N G T H G S L N H L L K V P
 1621 CATTCAACCAGCACCAACAATGGAACCCATGGTAGTTTAAACCATCTTCTGAAGGTGCC
 547 F Y E P S H A E E V S K F S V C G F A N
 1681 TTTTATGAGCCATCCCATGCAGAGGAGGTGTCAAAGTTTTCTGTTTGTGGCTTTGCTAA
 567 P L P T E S L D C F C P H L Q N S T Q L
 1741 TCCATTGCCACAGAGTCTCTTGACTGTTTCTGCCCTCACCTACAAATAGTACTCAGCT
 587 E Q V N Q M L N L T Q E E I T A T V K V
 1801 GGAACAAGTGAATCAGATGCTAAATCTCACCCAAGAAGAAATAACAGCAACAGTGAAAGT
 607 N L P F G R P R V L Q K N V D H C L L Y
 1861 AAATTTGCCATTTGGGAGGCCTAGGGTACTGCAGAAGAACGTGGACCACTGTCTCCTTTA
 627 H R E Y V S G F G K A M R M P M W S S Y
 1921 CCACAGGGAATATGTCAGTGGATTTGGAAAAGCTATGAGGATGCCCATGTGGAGTTCATA
 647 T V P Q L G D T S P L P P T V P D C L R
 1981 CACAGTCCCCCAGTTGGGAGACACATCGCCTCTGCCTCCCACTGTCCCAGACTGTCTGCG
 667 A D V R V P P S E S Q K C S F Y L A D K
 2041 GGCTGATGTCAGGGTTCCTCCTTCTGAGAGCCAAAATGTTTCCTTCTATTTAGCAGACAA

687 N I T H G F L Y P P A S N R T S D S Q Y
 2101 GAATATCACCCACGGCTTCCTCTATCCTCCTGCCAGCAATAGAACATCAGATAGCCAATA
 707 D A L I T S N L V P M Y E E F R K M W D
 2161 TGATGCTTTAATTACTAGCAATTTGGTACCTATGTATGAAGAATTGAGAAAAATGTGGGA
 727 Y F H S V L L I K H A T E R N G V N V V
 2221 CTA CTTCACAGTGTTCCTTCTTATAAAACATGCCACAGAAAGAAATGGAGTAAATGTGGT
 747 S G P I F D Y N Y D G H F D A P D E I T
 2281 TAGTGGACCAATATTTGATTATAATTATGATGGCCATTTTGATGCTCCAGATGAAATTAC
 767 K H L A N T D V P I P T H Y F V V L T S
 2341 CAAACATTTAGCCAACACTGATGTTCCCATCCCAACACACTACTTTGTGGTGCTGACCAG
 787 C K N K S H T P E N C P G W L D V L P F
 2401 TTGTAAAAACAAGAGCCACACACCGGAAAACCTGCCCTGGGTGGCTGGATGTCCTACCCCTT
 807 I I P H R P T N V E S C P E G K P E A L
 2461 TATCATCCCTCACCGACCTACCAACGTGGAGAGCTGTCCTGAAGGTAAACCAGAAGCTCT
 827 W V E E R F T A H I A R V R D V E L L T
 2521 TTGGGTTGAAGAAAGATTTACAGCTCACATTGCCCGGTCCGTGATGTAGAACTTCTCAC
 847 G L D F Y Q D K V Q P V S E I L Q L K T
 2581 TGGGCTTGACTTCTATCAGGATAAAGTGCAGCCTGTCTCTGAAATTTTGCAACTAAAGAC
 867 Y L P T F E T T I *
 2641 ATATTTACCAACATTTGAAACCACTATTTAACTtaataatgtctacttaatatataat
 2701 actgtataaagtaattttggcaaatataagtgatTTTTCTGGAGAATTGTAATAAAA
 2761 gTTTTctatTTTTccttaaaaaaaaaaacggaattccgggcttgggaggctgaggcagga
 2821 gactcgcttgaaccgggaggcagaggttgcagtgaagcaagattgcgccattgcactcc
 2881 agagcctgggtgacagagcaagactacatctcaaaaaataaataaaataaaaagtaa
 2941 caataaaaaataaaaagaacagcagagagaatgagcaaggagaaatgtcacaaactattgc
 3001 aaaatactgttacactgggttggctctccaagaagatactggaatctcttcagccatttg
 3061 cttttcagaagtagaaaccagcaaaccacctctaagcggagaacatacgattctttatta
 3121 agtagctctggggaaggaaagaataaaagttgatagctccctgattgggaaaaaatgcac
 3181 aattaataaagaatgaagatgaaagaaagcatgcttatgttgtaacacaaaaaaattca
 3241 caaacgttgggtggaaggaaaacagtatagaaaacattactttaactaaaagctggaaaaa
 3301 ttttcagttgggatgcgactgacaaaaagaacgggatttccaggcataaagttggcgtga
 3361 gctacagagggcaccatgtggctcagtgggaagacccttcaagattcaaagttccatttga
 3421 cagagcaaaggcacttcgcaaggagaagggtttaattatgggtccaaaagccaagtgg
 3481 aaagcgagcaatttgcagcataactgcttctcctagacagggtgagtgggcaaaatacg
 3541 acagtacacacagtgactattagccactgccagaaacaggctgaacagccctgggagaca
 3601 agggaaaggcaggtgggtgggagttgttcatggagagaaaggagagttttagaaccagcaca
 3661 tccactggagatgctggggccaccagacccctcccagtcataaagtcgtggtgcctcattt
 3721 gatctcagcctcatcatgaccctggagagaccctgataccatctgccagtcctccgcagc

3781 ttaggcactccttgccatcaacctgaccccccgagtgggttctccaggctccctgccccac
 3841 ccattcaggccggaattc

Figure 2B: The cDNA (SEQ ID. NO. : 746) and amino acid sequence (SEQ ID. NO. : 745) of 161P2F10B variant 1. The 3858 nucleotide sequence of 161P2F10B variant 1 is shown. The start methionine is underlined. The open reading frame extends from nucleic acid 44-2671 including the stop codon.

1	M E S T L T
1	ctacttttattctgataaaacaggtctatgcagctaccaggacaATGGAATCTACGTTGAC
7	L A T E Q P V K K N T L K K Y K I A C I
61	TTTAGCAACGGAACAACCTGTTAAGAAGAACACTCTTAAGAAATATAAAATAGCTTGCAT
27	V L L A L L V I M S L G L G L G L G L R
121	TGTTCTTCTTGCTTTGCTGGTGATCATGTCACTTGGATTAGGCCTGGGGCTTGGACTCAG
47	K L E K Q G S C R K K C F D A S F R G L
181	GAAACTGGAAAAGCAAGGCAGCTGCAGGAAGAAGTGCTTTGATGCATCATTTAGAGGACT
67	E N C R C D V A C K D R G D C C W D F E
241	GGAGAACTGCCGGTGTGATGTGGCATGTAAAGACCGAGGTGATTGCTGCTGGGATTTTGA
87	D T C V E S T R I W M C N K F R C G E T
301	AGACACCTGTGTGGAATCAACTCGAATATGGATGTGCAATAAATTTTCGTTGTGGAGAGAC
107	R L E A S L C S C S D D C L Q R K D C C
361	CAGATTAGAGGCCAGCCTTTGCTCTTGTTTCAGATGACTGTTTGCAGAGGAAAGATTGCTG
127	A D Y K S V C Q G E T S W L E E N C D T
421	TGCTGACTATAAGAGTGTGTTGCCAAGGAGAAACCTCATGGCTGGAAGAAAACCTGTGACAC
147	A Q Q S Q C P E G F D L P P V I L F S M
481	AGCCCAGCAGTCTCAGTGCCCAAGGGTTTGACCTGCCACCAGTTATCTTGTTTTCTAT
167	D G F R A E Y L Y T W D T L M P N I N K
541	GGATGGATTTAGAGCTGAATATTTATACACATGGGATACTTTAATGCCAAATATCAATAA
187	L K T C G I H S K Y M R A M Y P T K T F
601	ACTGAAAACATGTGGAATTCATTCAAATAACATGAGAGCTATGTATCCTACCAAAACCTT
207	P N H Y T I V T G L Y P E S H G I I D N
661	CCCAAATCATTACACCATTTGTCACGGGCTTGTATCCAGAGTCACATGGCATCATTGACAA
227	N M Y D V N L N K N F S L S S K E Q N N
721	TAATATGTATGATGTAAATCTCAACAAGAATTTTTCACTTTCTTCAAAGGAACAAAATAA
247	P A W W H G Q P M W L T A M Y Q G L K A
781	TCCAGCCTGGTGGCATGGGCAACCAATGTGGCTGACAGCAATGTATCAAGGTTTAAAGC
267	A T Y F W P G S E V A I N G S F P S I Y
841	CGCTACCTACTTTTGGCCCGGATCAGAAGTGGCTATAAATGGCTCCTTTTCCTTCCATATA

287 M P Y N G S V P F E E R I S T L L K W L
 901 CATGCCTTACAACGGAAGTGTCCCATTGGAAGAGAGGATTTCTACACTGTTAAAATGGCT
 307 D L P K A E R P R F Y T M Y F E E P D S
 961 GGACCTGCCCCAAGCTGAAAGACCCAGGTTTTATACCATGTATTTTGAAGAACCTGATTC
 327 S G H A G G P V S A R V I K A L Q V V D
 1021 CTCTGGACATGCAGGTGGACCAGTCAGTGCCAGAGTAATTAAAGCCTTACAGGTAGTAGA
 347 H A F G M L M E G L K Q R N L H N C V N
 1081 TCATGCTTTTGGGATGTTGATGGAAGGCCTGAAGCAGCGGAATTTGCACAACCTGTGTCAA
 367 I I L L A D H G M D Q T Y C N K M E Y M
 1141 TATCATCCTTCTGGCTGACCATGGAATGGACCAGACTTATTGTAACAAGATGGAATACAT
 387 T D Y F P R I N F F Y M Y E G P A P R I
 1201 GACTGATTATTTTCCCAGAATAAACTTCTTCTACATGTACGAAGGGCCTGCCCCCGCAT
 407 R A H N I P H D F F S F N S E E I V R N
 1261 CCGAGCTCATAATATACCTCATGACTTTTTTAGTTTTAATTCTGAGGAAATTGTTAGAAA
 427 L S C R K P D Q H F K P Y L T P D L P K
 1321 CCTCAGTTGCCGAAAACCTGATCAGCATTTCAAGCCCTATTTGACTCCTGATTTGCCAAA
 447 R L H Y A K N V R I D K V H L F V D Q Q
 1381 GCGACTGCACTATGCCAAGAACGTGAGAATCGACAAAGTTCATCTCTTTGTGGATCAACA
 467 W L A V R S K S N T N C G G G N H G Y N
 1441 GTGGCTGGCTGTTAGGAGTAAATCAAATACAAATTGTGGAGGAGGCAACCATGGTTATAA
 487 N E F R S M E A I F L A H G P S F K E K
 1501 CAATGAGTTTAGGAGCATGGAGGCTATCTTTCTGGCACATGGACCCAGTTTTAAAGAGAA
 507 T E V E P F E N I E V Y N L M C D L L R
 1561 GACTGAAGTTGAACCATTTGAAAATATTGAAGTCTATAACCTAATGTGTGATCTTCTACG
 527 I Q P A P N N G T H G S L N H L L K V P
 1621 CATTCAACCAGCACCAACAATGGAACCCATGGTAGTTTAAACCATCTTCTGAAGGTGCC
 547 F Y E P S H A E E V S K F S V C G F A N
 1681 TTTTATAGCCATCCCATGCAGAGGAGGTGTCAAAGTTTTCTGTTTGTGGCTTTGCTAA

 567 P L P T E S L D C F C P H L Q N S T Q L
 1741 TCCATTGCCCACAGAGTCTCTTGACTGTTTCTGCCCTCACCTACAAAATAGTACTCAGCT
 587 E Q V N Q M L N L T Q E E I T A T V K V
 1801 GGAACAAGTGAATCAGATGCTAAATCTCACCCAAGAAGAAATAACAGCAACAGTGAAAGT
 607 N L P F G R P R V L Q K N V D H C L L Y
 1861 AAATTTGCCATTTGGGAGGCCTAGGGTACTGCAGAAGAACGTGGACCACTGTCTCCTTTA
 627 H R E Y V S G F G K A M R M P M W S S Y
 1921 CCACAGGGAATATGTCAGTGGATTTGGAAAAGCTATGAGGATGCCCATGTGGAGTTCATA
 647 T V P Q L G D T S P L P P T V P D C L R
 1981 CACAGTCCCCCAGTTGGGAGACACATCGCCTCTGCCTCCCACTGTCCCAGACTGTCTGCG

667 A D V R V P P S E S Q K C S F Y L A D K
 2041 GGCTGATGTCAGGGTTCCTCCTTCTGAGAGCCAAAAATGTTCTTCTATTTAGCAGACAA
 687 N I T H G F L Y P P A S N R T S D S Q Y
 2101 GAATATCACCCACGGCTTCCTCTATCCTCCTGCCAGCAATAGAACATCAGATAGCCAATA
 707 D A L I T S N L V P M Y E E F R K M W D
 2161 TGATGCTTTAATTACTAGCAATTTGGTACCTATGTATGAAGAATTCAGAAAAATGTGGGA
 727 Y F H S V L L I K H A T E R N G V N V V
 2221 CTACTTCCACAGTGTTCCTTCTTATAAAACATGCCACAGAAAGAAATGGAGTAAATGTGGT
 747 S G P I F D Y N Y D G H F D A P D E I T
 2281 TAGTGGACCAATATTTGATTATAATTATGATGGCCATTTTGATGCTCCAGATGAAATTAC
 767 K H L A N T D V P I P T H Y F V V L T S
 2341 CAAACATTTAGCCAACACTGATGTTCCCATCCCAACACACTACTTTGTGGTGCTGACCAG
 787 C K N K S H T P E N C P G W L D V L P F
 2401 TTGTAAAAACAAGAGCCACACACCGGAAACTGCCCTGGGTGGCTGGATGTCCTACCCTT
 807 I I P H R P T N V E S C P E G K P E A L
 2461 TATCATCCCTCACCGACCTACCAACGTGGAGAGCTGTCCTGAAGGTAAACCAGAAGCTCT
 827 W V E E R F T A H I A R V R D V E L L T
 2521 TTGGGTTGAAGAAAGATTTACAGCTCACATTGCCCGGGTCCGTGATGTAGAAGTTCTCAC
 847 G L D F Y Q D K V Q P V S E I L Q L K T
 2581 TGGGCTTGACTTCTATCAGGATAAAGTGCAGCCTGTCTCTGAAATTTTGCAACTAAAGAC
 867 Y L P T F E T T I *
 2641 ATATTTACCAACATTTGAAACCACTATTTAACTtaataatgtctacttaatatataat
 2701 actgtataaagtaattttggcaaaatataagtgattttttctggagaattgtaaaataaa
 2761 gttttctatttttccttaaaaaaaaaaccggaattccgggcttgggaggctgaggcagga
 2821 gactcgcttgaacccgggaggcagaggttgcagtgagccaagattgcgccattgcactcc
 2881 agagcctgggtgacagagcaagactacatctcaaaaaataaataaaataaaaagtaa
 2941 caataaaaaataaaaagaacagcagagagaatgagcaaggagaaatgtcacaaactattgc
 3001 aaaatactgttacactgggttggctctccaagaagatactggaatctcttcagccatttg
 3061 cttttcagaagtagaaaccagcaaaccacctctaagcggagaacatacgattctttatta
 3121 agtagctctggggaaggaaagaataaaagttgatagctccctgattgggaaaaaatgcac
 3181 aattaataaagaatgaagatgaaagaaagcatgcttatgttgtaacacaaaaaaattca
 3241 caaacgttgggtggaaggaaaacagtatagaaaacattactttaactaaaagctggaaaaa
 3301 ttttcagttgggatgcgactgacaaaaagaacgggatttccaggcataaagttggcgtga
 3361 gctacagagggcaccatgtggctcagtggaagacccttcaagattcaaagttccatttga
 3421 cagagcaaaggcacttcgcaaggagaagggttttaattatgggtccaaaagccaagtgg
 3481 aaagcgagcaatttgcagcataactgcttctcctagacagggtgagtgggcaaaatacg
 3541 acagtacacacagtgactattagccactgccagaaacagggtgaacagccctgggagaca
 3601 agggaaggcaggtgggtgggagttgttcatggagagaaaggagagttttagaaccagcaca

3661 tccactggagatgctgggcccaccagacccctcccagtcataaagtctggtgcctcattt
3721 gatctcagcctcatcatgaccctggagagaccctgataccatctgccagtccccgacagc
3781 ttaggcactccttgccatcaacctgacccccgagtggttctccaggtccctgccccac
3841 ccattcaggccggaattc

Figure 3A. Amino acid sequence of 161P2F10B (SEQ ID. NO. : 747). The 161P2F10B protein has 875 amino acids.

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1 MESTLTLATE QPVKKNTLKK YKIACIVLLA LLVIMSLGLG LGLGLRKLEK QGSCRKKCFD
61 ASFRGLENCR CDVACKDRGD CCWDFEDTCV ESTRIWMCNK FRCGETRLEA SLCSDDCL
121 QKKDCCADYK SVCQGETSWL EENCDAQQS QCPEGFDLPP VILFSMDGFR AEYLYTWDTL
181 MPNINKLKTC GIHSKYMRAM YPTKTFPNHY TIVTGLYPES HGIIDNNMYD VNLNKNFSL
241 SKEQNNPAWW HGQPMWLTAM YQGLKAATYF WPGSEVAING SFPSIYMPYN GSVPFEEERIS
301 TLLKWLDPK AERPRFYTM YFEEDSSGHA GGPVSARVIK ALQVVDHAFG MLMEGLKQRN
361 LHNCVNIILL ADHGMDQTYC NKMEYMTDYF PRINFFYMYE GPAPRIRAHN IPHDDFFSFNS
421 EEIVRNLSR KPDQHFQPYL TPDLPKRLHY AKNVRIDKVH LFVDQQLAV RSKSNTNCGG
481 GNHGYNNEFR SMEAIFLAHG PSFKEKTEVE PFENIEVYNL MCDLLRIQPA PNNGTHGSLN
541 HLLKVPFYEP SHAEVSKFS VCGFANPLPT ESLDCFCPHL QNSTQLEQVN QMLNLTQEEI
601 TATVKVNLPF GRPRVLQKNV DHCLLYHREY VSGFGKAMRM PMWSSYTVPQ LGDTSPLPPT
661 VPDCLRADVR VPPSESQKCS FYLADKNITH GFLYPPASNR TSDSQYDALI TSNLVPYEE
721 FRKMWDYFHS VLLIKHATER NGVNVVSGPI FDYNDGHFD APDEITKHLA NTDVPIPTHY
781 FVVLTSCKNK SHTPENCPGW LDVLPFIIPH RPTNVESCPE GKPEALWVEE RFTAHIAVR
841 DVELLTGLDF YQDKVQPVSE ILQLKTYLPT FETTI

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Figure 3B. Amino acid sequence of 161P2F10B variant 1 (SEQ ID. NO. : 748). The 161P2F10B variant 1 protein has 875 amino acids.

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1 MESTLTLATE QPVKKNTLKK YKIACIVLLA LLVIMSLGLG LGLGLRKLEK QGSCRKKCFD
61 ASFRGLENCR CDVACKDRGD CCWDFEDTCV ESTRIWMCNK FRCGETRLEA SLCSDDCL
121 QRKDCCADYK SVCQGETSWL EENCDAQQS QCPEGFDLPP VILFSMDGFR AEYLYTWDTL
181 MPNINKLKTC GIHSKYMRAM YPTKTFPNHY TIVTGLYPES HGIIDNNMYD VNLNKNFSL
241 SKEQNNPAWW HGQPMWLTAM YQGLKAATYF WPGSEVAING SFPSIYMPYN GSVPFEEERIS
301 TLLKWLDPK AERPRFYTM YFEEDSSGHA GGPVSARVIK ALQVVDHAFG MLMEGLKQRN
361 LHNCVNIILL ADHGMDQTYC NKMEYMTDYF PRINFFYMYE GPAPRIRAHN IPHDDFFSFNS
421 EEIVRNLSR KPDQHFQPYL TPDLPKRLHY AKNVRIDKVH LFVDQQLAV RSKSNTNCGG
481 GNHGYNNEFR SMEAIFLAHG PSFKEKTEVE PFENIEVYNL MCDLLRIQPA PNNGTHGSLN
541 HLLKVPFYEP SHAEVSKFS VCGFANPLPT ESLDCFCPHL QNSTQLEQVN QMLNLTQEEI
601 TATVKVNLPF GRPRVLQKNV DHCLLYHREY VSGFGKAMRM PMWSSYTVPQ LGDTSPLPPT
661 VPDCLRADVR VPPSESQKCS FYLADKNITH GFLYPPASNR TSDSQYDALI TSNLVPYEE
721 FRKMWDYFHS VLLIKHATER NGVNVVSGPI FDYNDGHFD APDEITKHLA NTDVPIPTHY
781 FVVLTSCKNK SHTPENCPGW LDVLPFIIPH RPTNVESCPE GKPEALWVEE RFTAHIAVR
841 DVELLTGLDF YQDKVQPVSE ILQLKTYLPT FETTI

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Figure 4

Figure 4A. Amino acid alignment of 161P2F10B (SEQ. ID. No. 747) with ENPP3 (SEQ. ID. No. 765).

161P2F10B	m e s t l t l a t e q p p	v k k n t l k k y k i a c i v l l a l l v i m s l g l g	40
ENPP3	m e s t l t l a t e q p p	v k k n t l k k y k i a c i v l l a l l v i m s l g l g	40
161P2F10B	l g l g l r k l e k q g s	s c r k k c f d a s f r g l e n c r c d v a c k d r g d	80
ENPP3	l g l g l r k l e k q g s	s c r k k c f d a s f r g l e n c r c d v a c k d r g d	80
161P2F10B	c c w d f e d t c v e s t	t r i w m c n k f r c g e t r l e a s l c s c s d d c l	120
ENPP3	c c w d f e d t c v e s t	t r i w m c n k f r c g e t r l e a s l c s c s d d c l	120
161P2F10B	q k k d c c a d y k s v	c q g e t s w l e e n c d t a q q s q c p e g f d l p p	160
ENPP3	q k k d c c a d y k s v	c q g e t s w l e e n c d t a q q s q c p e g f d l p p	160
161P2F10B	v i l f s m d g f r a e y	l y t w d t l m p n i n k l k t c g i h s k y m r a m	200
ENPP3	v i l f s m d g f r a e y	l y t w d t l m p n i n k l k t c g i h s k y m r a m	200
161P2F10B	y p t k t f p n h y t i v	t g l y p e s h g i i d n n m y d v n l n k n f s l s	240
ENPP3	y p t k t f p n h y t i v	t g l y p e s h g i i d n n m y d v n l n k n f s l s	240
161P2F10B	s k e q n n p a w w h g q	p m w l t a m y q g l k a a t y f w p g s e v a i n g	280
ENPP3	s k e q n n p a w w h g q	p m w l t a m y q g l k a a t y f w p g s e v a i n g	280
161P2F10B	s f p s i y m p y n g s v	p f e e r i s t l l k w l d l p k a e r p r f y t m y	320
ENPP3	s f p s i y m p y n g s v	p f e e r i s t l l k w l d l p k a e r p r f y t m y	320
161P2F10B	f e e p d s s g h a g g p p	v s a r v i k a l q v v d h a f g m l m e g l k q r n	360
ENPP3	f e e p d s s g h a g g p p	v s a r v i k a l q v v d h a f g m l m e g l k q r n	360
161P2F10B	l h n c v n i i l l a d h	g m d q t y c n k m e y m t d y f p r i n f f y m y e	400
ENPP3	l h n r v n i i l l a d h	g m d q t y c n k m e y m t d y f p r i n f f y m y e	400
161P2F10B	g p a p r i r a h n i p h	d f f s f n s e e i v r n l s c r k p d q h f k p y l	440
ENPP3	g p a p r i r a h n i p h	d f f s f n s e e i v r n l s c r k p d q h f k p y l	440
161P2F10B	t p d l p k r l h y a k n	v r i d k v h l f v d q q w l a v r s k s n t n c g g	480
ENPP3	t p d l p k r l h y a k n	v r i d k v h l f v d q q w l a v r s k s n t n c g g	480

161P2F10B	gnhgy	nne	f	r	s	m	e	a	i	f	l	a	h	g	p	s	f	k	e	k	t	e	v	e	p	f	e	n	i	e	v	y	n	l	520		
ENPP3	gnhgy	nne	f	r	s	m	e	a	i	f	l	a	h	g	p	s	f	k	e	k	t	e	v	e	p	f	e	n	i	e	v	y	n	l	520		
161P2F10B	mcdll	r	i	q	p	a	p	n	n	g	t	h	g	s	l	n	h	l	l	k	v	p	f	y	e	p	s	h	a	e	e	v	s	k	f	s	560
ENPP3	mcdll	r	i	q	p	a	p	n	n	g	t	h	g	s	l	n	h	l	l	k	v	p	f	y	e	p	s	h	a	e	e	v	s	k	f	s	560
161P2F10B	vcgfa	n	p	l	p	t	e	s	l	d	c	f	c	p	h	l	q	n	s	t	q	l	e	q	v	n	q	m	l	n	l	t	q	e	e	i	600
ENPP3	vcgfa	n	p	l	p	t	e	s	l	d	c	f	c	p	h	l	q	n	s	t	q	l	e	q	v	n	q	m	l	n	l	t	q	e	e	i	600
161P2F10B	tatvk	v	n	l	p	f	g	r	p	r	v	l	q	k	n	v	d	h	c	l	l	y	h	r	e	y	v	s	g	f	g	k	a	m	r	m	640
ENPP3	tatvk	v	n	l	p	f	g	r	p	r	v	l	q	k	n	v	d	h	c	l	l	y	h	r	e	y	v	s	g	f	g	k	a	m	r	m	640
161P2F10B	pmwss	y	t	v	p	q	l	g	d	t	s	p	l	p	p	t	v	p	d	c	l	r	a	d	v	r	v	p	p	s	e	s	q	k	c	s	680
ENPP3	pmwss	y	t	v	p	q	l	g	d	t	s	p	l	p	p	t	v	p	d	c	l	r	a	d	v	r	v	p	p	s	e	s	q	k	c	s	680
161P2F10B	fylad	k	n	i	t	h	g	f	l	y	p	p	a	s	n	r	t	s	d	s	q	y	d	a	l	i	t	s	n	l	v	p	m	y	e	e	720
ENPP3	fylad	k	n	i	t	h	g	f	l	y	p	p	a	s	n	r	t	s	d	s	q	y	d	a	l	i	t	s	n	l	v	p	m	y	e	e	720
161P2F10B	frkmw	d	y	f	h	s	v	l	l	i	k	h	a	t	e	r	n	g	v	n	v	v	s	g	p	i	f	d	y	n	y	d	g	h	f	d	760
ENPP3	frkmw	d	y	f	h	s	v	l	l	i	k	h	a	t	e	r	n	g	v	n	v	v	s	g	p	i	f	d	y	n	y	d	g	h	f	d	760
161P2F10B	apdei	t	k	h	l	a	n	t	d	v	p	i	p	t	h	y	f	v	v	l	t	s	c	k	n	k	s	h	t	p	e	n	c	p	g	w	800
ENPP3	apdei	t	k	h	l	a	n	t	d	v	p	i	p	t	h	y	f	v	v	l	t	s	c	k	n	k	s	h	t	p	e	n	c	p	g	w	800
161P2F10B	ldvlp	f	i	i	p	h	r	p	t	n	v	e	s	c	p	e	g	k	p	e	a	l	w	v	e	e	r	f	t	a	h	i	a	r	v	r	840
ENPP3	ldvlp	f	i	i	p	h	r	p	t	n	v	e	s	c	p	e	g	k	p	e	a	l	w	v	e	e	r	f	t	a	h	i	a	r	v	r	840
161P2F10B	dve	l	l	t	g	l	d	f	y	q	d	k	v	q	p	v	s	e	i	l	q	l	k	t	y	l	p	t	f	e	t	t	i		875		
ENPP3	dve	l	l	t	g	l	d	f	y	q	d	k	v	q	p	v	s	e	i	l	q	l	k	t	y	l	p	t	f	e	t	t	i		875		

Figure 4b. Amino acid alignment of 161P2F10B (SEQ. ID. No. 747) with 161P2F10B variant 1 (SEQ. ID. No. 748).

161P2F10B	mestl	t	l	a	t	e	q	p	v	k	n	t	l	k	y	k	i	a	c	i	v	l	a	l	v	i	m	s	l	g	l	g	40					
161P2F10B variant 1	mestl	t	l	a	t	e	q	p	v	k	n	t	l	k	y	k	i	a	c	i	v	l	a	l	v	i	m	s	l	g	l	g	40					
161P2F10B	lg	l	g	l	r	k	l	e	k	q	g	s	c	r	k	k	c	f	d	a	s	f	r	g	l	e	n	c	r	d	v	a	c	k	d	r	g	80
161P2F10B variant 1	lg	l	g	l	r	k	l	e	k	q	g	s	c	r	k	k	c	f	d	a	s	f	r	g	l	e	n	c	r	d	v	a	c	k	d	r	g	80

161P2F10B	ccwdfedtccvestriwmcnkfrcgetrleascscsddcl	120
161P2F10B variant 1	ccwdfedtccvestriwmcnkfrcgetrleascscsddcl	120
161P2F10B	qk k d c c a d y k s v c g g e t s w l e e n c d t a q q s q c p e g f d l p p	160
161P2F10B variant 1	q r k d c c a d y k s v c g g e t s w l e e n c d t a q q s q c p e g f d l p p	160
161P2F10B	v i l f s m d g f r a e y l y t w d t l m p n i n k l k t c g i h s k y m r a m	200
161P2F10B variant 1	v i l f s m d g f r a e y l y t w d t l m p n i n k l k t c g i h s k y m r a m	200
161P2F10B	y p t k t f p n h y t i v t g l y p e s h g i i d n n m y d v n l n k n f s l s	240
161P2F10B variant 1	y p t k t f p n h y t i v t g l y p e s h g i i d n n m y d v n l n k n f s l s	240
161P2F10B	s k e q n n p a w w h g q p m w l t a m y q g l k a a t y f w p g s e v a i n g	280
161P2F10B variant 1	s k e q n n p a w w h g q p m w l t a m y q g l k a a t y f w p g s e v a i n g	280
161P2F10B	s f p s i y m p y n g s v p f e e r i s t l l k w l d l p k a e r p r f y t m y	320
161P2F10B variant 1	s f p s i y m p y n g s v p f e e r i s t l l k w l d l p k a e r p r f y t m y	320
161P2F10B	f e e p d s s g h a g g p v s a r v i k a l q v v d h a f g m l m e g l k q r n	360
161P2F10B variant 1	f e e p d s s g h a g g p v s a r v i k a l q v v d h a f g m l m e g l k q r n	360
161P2F10B	l h n c v n i i l l a d h g m d q t y c n k m e y m t d y f p r i n f f y m y e	400
161P2F10B variant 1	l h n r v n i i l l a d h g m d q t y c n k m e y m t d y f p r i n f f y m y e	400
161P2F10B	g p a p r i r a h n i p h d f f s f n s e e i v r n l s c r k p d q h f k p y l	440
161P2F10B variant 1	g p a p r i r a h n i p h d f f s f n s e e i v r n l s c r k p d q h f k p y l	440
161P2F10B	t p d l p k r l h y a k n v r i d k v h l f v d q q w l a v r s k s n t n c g g	480
161P2F10B variant 1	t p d l p k r l h y a k n v r i d k v h l f v d q q w l a v r s k s n t n c g g	480
161P2F10B	g n h g y n n e f r s m e a i f l a h g p s f k e k t e v e p f e n i e v y n l	520
161P2F10B variant 1	g n h g y n n e f r s m e a i f l a h g p s f k e k t e v e p f e n i e v y n l	520
161P2F10B	m c d l l r i q p a p n n g t h g s l n h l l k v p f y e p s h a e e v s k f s	560
161P2F10B variant 1	m c d l l r i q p a p n n g t h g s l n h l l k v p f y e p s h a e e v s k f s	560
161P2F10B	v c g f a n p l p t e s l d c f c p h l q n s t q l e q v n q m l n l t q e e i	600
161P2F10B variant 1	v c g f a n p l p t e s l d c f c p h l q n s t q l e q v n q m l n l t q e e i	600

161P2F10B	t a t v k v n l p f g r p r v l q k n v d h c l l y h r e y v s g f g k a m r m	640
161P2F10B variant 1	t a t v k v n l p f g r p r v l q k n v d h c l l y h r e y v s g f g k a m r m	640
161P2F10B	p m w s s y t v p q l g d t s p l p p t v p d c l r a d v r v p p s e s q k c s	680
161P2F10B variant 1	p m w s s y t v p q l g d t s p l p p t v p d c l r a d v r v p p s e s q k c s	680
161P2F10B	f y l a d k n i t h g f l y p p a s n r t s d s q y d a l i t s n l v p m y e e	720
161P2F10B variant 1	f y l a d k n i t h g f l y p p a s n r t s d s q y d a l i t s n l v p m y e e	720
161P2F10B	f r k m w d y f h s v l l i k h a t e r n g v n v v s g p i f d y n y d g h f d	760
161P2F10B variant 1	f r k m w d y f h s v l l i k h a t e r n g v n v v s g p i f d y n y d g h f d	760
161P2F10B	a p d e i t k h l a n t d v p i p t h y f v v l t s c k n k s h t p e n c p g w	800
161P2F10B variant 1	a p d e i t k h l a n t d v p i p t h y f v v l t s c k n k s h t p e n c p g w	800
161P2F10B	l d v l p f i i p h r p t n v e s c p e g k p e a l w v e e r f t a h i a r v r	840
161P2F10B variant 1	l d v l p f i i p h r p t n v e s c p e g k p e a l w v e e r f t a h i a r v r	840
161P2F10B	d v e l l t g l d f y q d k v q p v s e i l q l k t y l p t f e t t i	875
161P2F10B variant 1	d v e l l t g l d f y q d k v q p v s e i l q l k t y l p t f e t t i	875

4C) Alignment of 161P2F10B (SEQ. ID. No. 749) and SNP variant 2 (SEQ. ID. No. 750) carrying a T to P mutation at position 874.

```

Query: 492 MEAIFLAHGSPFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTHGSLNHLLKVPFYEPS 551
          MEAIFLAHGSPFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTHGSLNHLLKVPFYEPS
Sbjct: 1   MEAIFLAHGSPFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTHGSLNHLLKVPFYEPS 60

Query: 552 HAEVSKFSVCGFANPLPTESLDCFCPHLQNSTQLEQVNQMLNLTQEEITATVKVNLPPFG 611
          HAEVSKFSVCGFANPLPTESLDCFCPHLQNSTQLEQVNQMLNLTQEEITATVKVNLPPFG
Sbjct: 61  HAEVSKFSVCGFANPLPTESLDCFCPHLQNSTQLEQVNQMLNLTQEEITATVKVNLPPFG 120

Query: 612 RPRVLQKNVDHCLLYHREYVSGFGKAMRMPMWSSYTPVQLGDTSPLPPTVPDCLRADVRV
671
          RPRVLQKNVDHCLLYHREYVSGFGKAMRMPMWSSYTPVQLGDTSPLPPTVPDCLRADVRV
Sbjct: 121 RPRVLQKNVDHCLLYHREYVSGFGKAMRMPMWSSYTPVQLGDTSPLPPTVPDCLRADVRV 180

Query: 672 PPSEQKCSFYLDKNITHGFLYPASNRTSDSQYDALITSNLVPMYEEFRKMWDYFHVS 731
          PPSEQKCSFYLDKNITHGFLYPASNRTSDSQYDALITSNLVPMYEEFRKMWDYFHVS
Sbjct: 181 PPSEQKCSFYLDKNITHGFLYPASNRTSDSQYDALITSNLVPMYEEFRKMWDYFHVS 240

Query: 732 LLIKHATERNGVNVVSGPIFDYNYDGHFDAPDEITKHLANTDVPIPTHYFVVLTSCKNKS 791
          LLIKHATERNGVNVVSGPIFDYNYDGHFDAPDEITKHLANTDVPIPTHYFVVLTSCKNKS
Sbjct: 241 LLIKHATERNGVNVVSGPIFDYNYDGHFDAPDEITKHLANTDVPIPTHYFVVLTSCKNKS 300

Query: 792 HTPENCPGWLDVLPFIIPHRPTNVESCPEGKPEALWVEERFTAHIARVRDVELLTGLDY 851
          HTPENCPGWLDVLPFIIPHRPTNVESCPEGKPEALWVEERFTAHIARVRDVELLTGLDY
Sbjct: 301 HTPENCPGWLDVLPFIIPHRPTNVESCPEGKPEALWVEERFTAHIARVRDVELLTGLDY 360

Query: 852 QDKVQPVSEILQLKTYLPTFETTI 875
          QDKVQPVSEILQLKTYLPTFET I
Sbjct: 361 QDKVQPVSEILQLKTYLPTFETPI 384

```

Figure 5: 161P2F10B Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

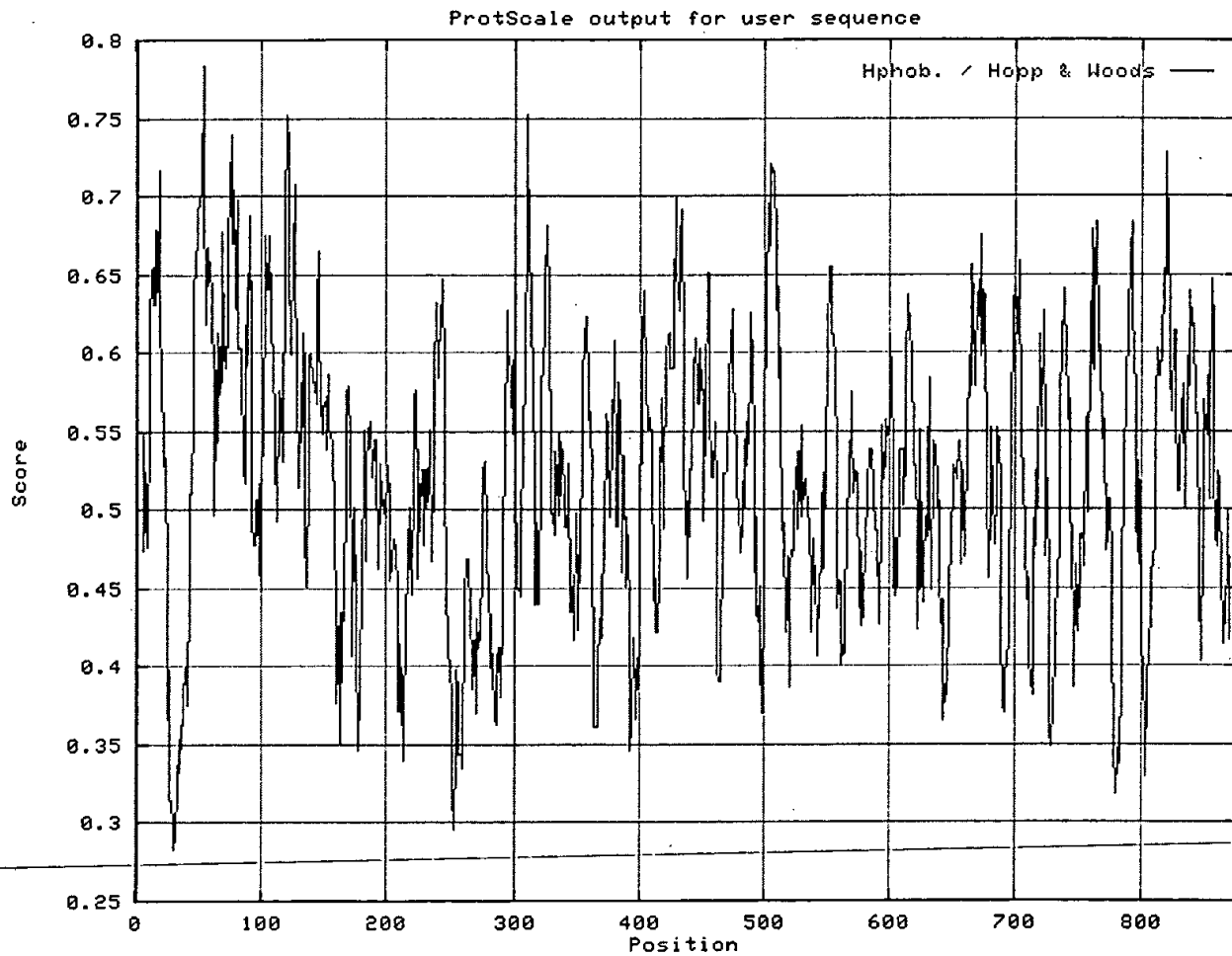


Figure 6: 161P2F10B Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

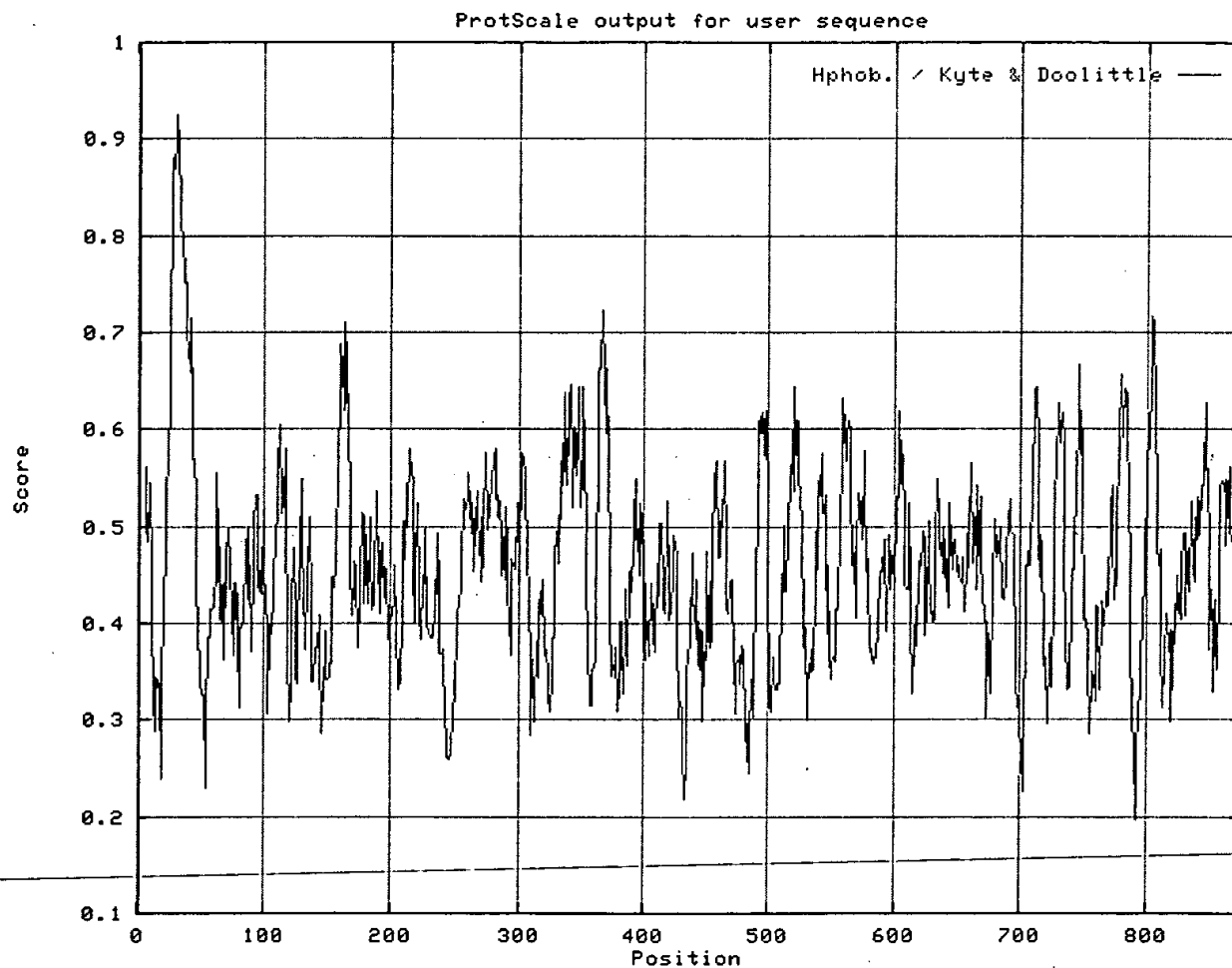


Figure 7: 161P2F10B % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

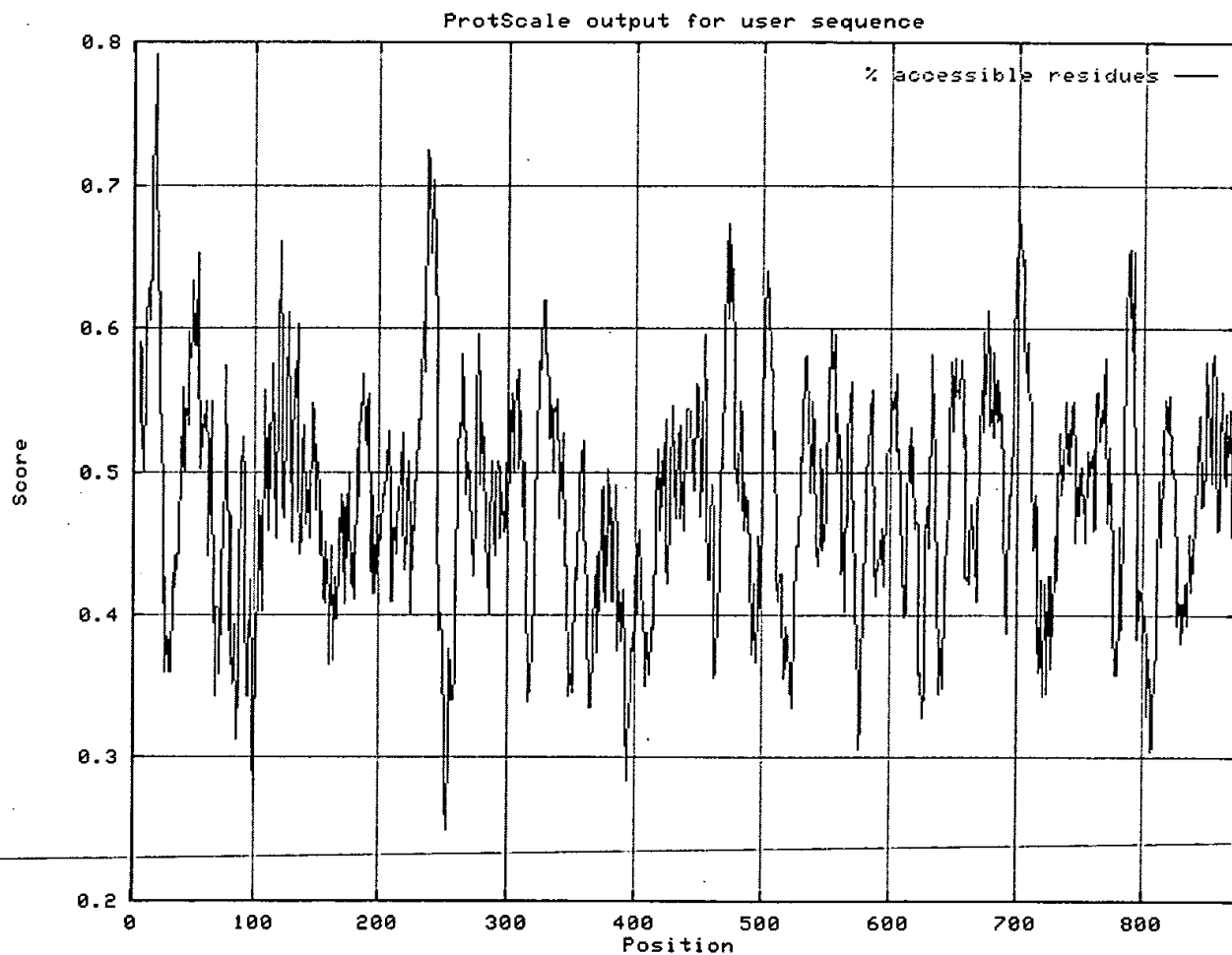


Figure 8: 161P2F10B Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.

Int. J. Pept. Protein Res. 32:242-255)

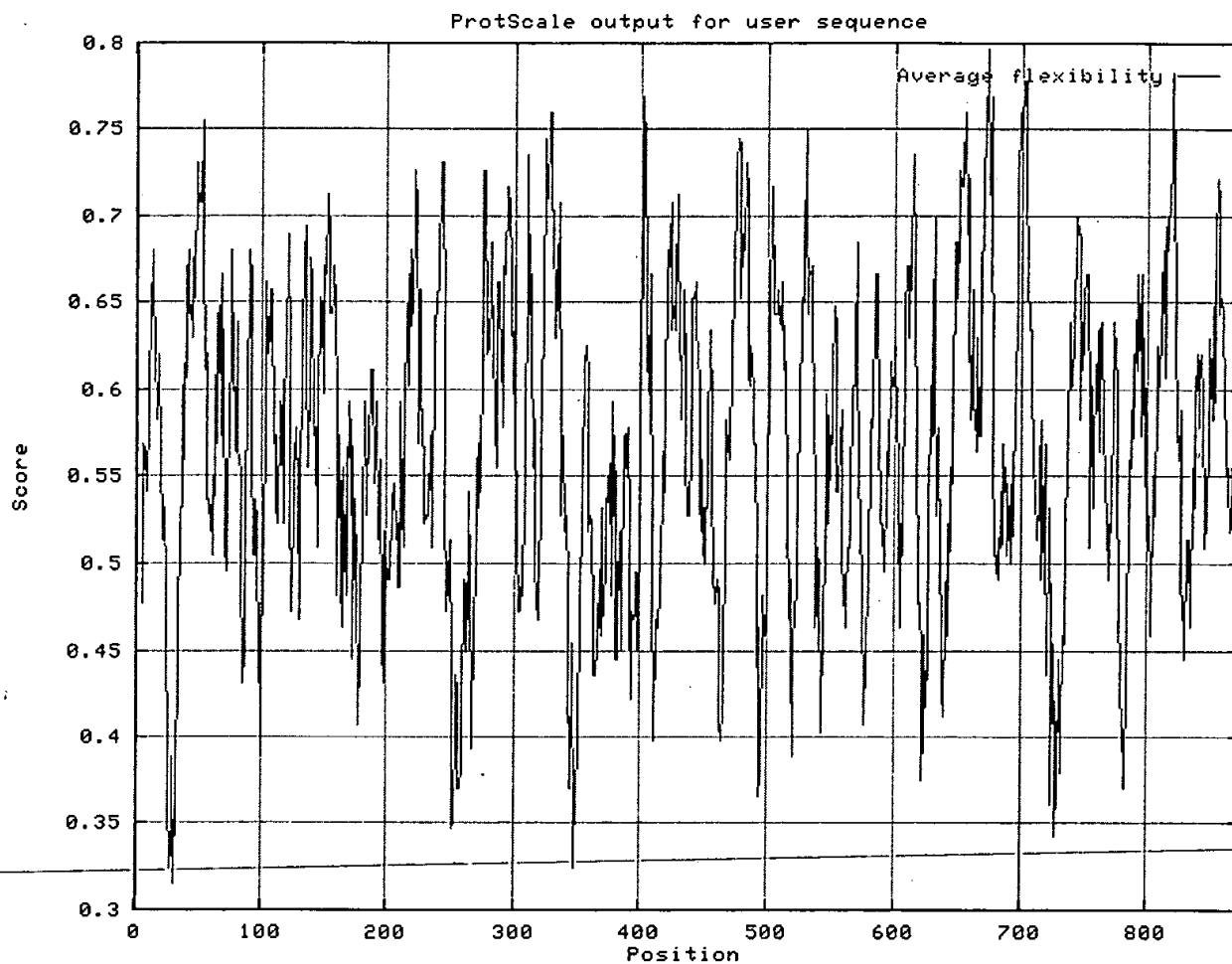


Figure 9: 161P2F10B Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

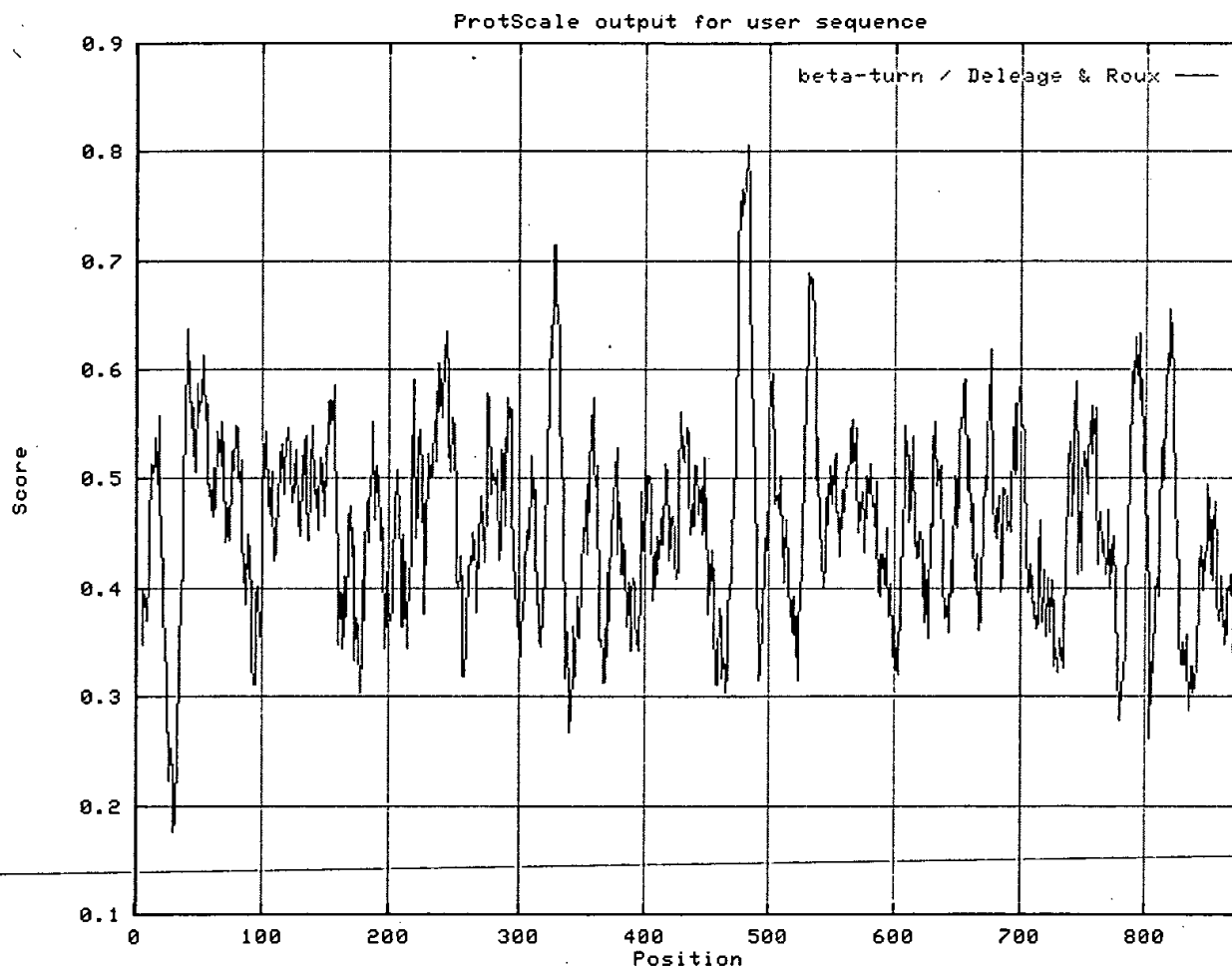


Figure 10: Expression of 161P2F10B by RT-PCR



- M = Marker
- Vital Pool 1
 - 2) Vital Pool 2
 - 3) Xenograft Pool
 - 4) Prostate Cancer Pool
 - Kidney Cancer Pool
 - Colon Cancer Pool
 - Lung Cancer Pool
 - Ovary Cancer Pool
 - Breast Cancer Pool
 - Metastasis Pool
 - Pancreas cancer Pool
 - Prostate Met to LN #1
 - Prostate Met to LN #2

Figure 11: Expression of 161P2F10B in Normal Tissues

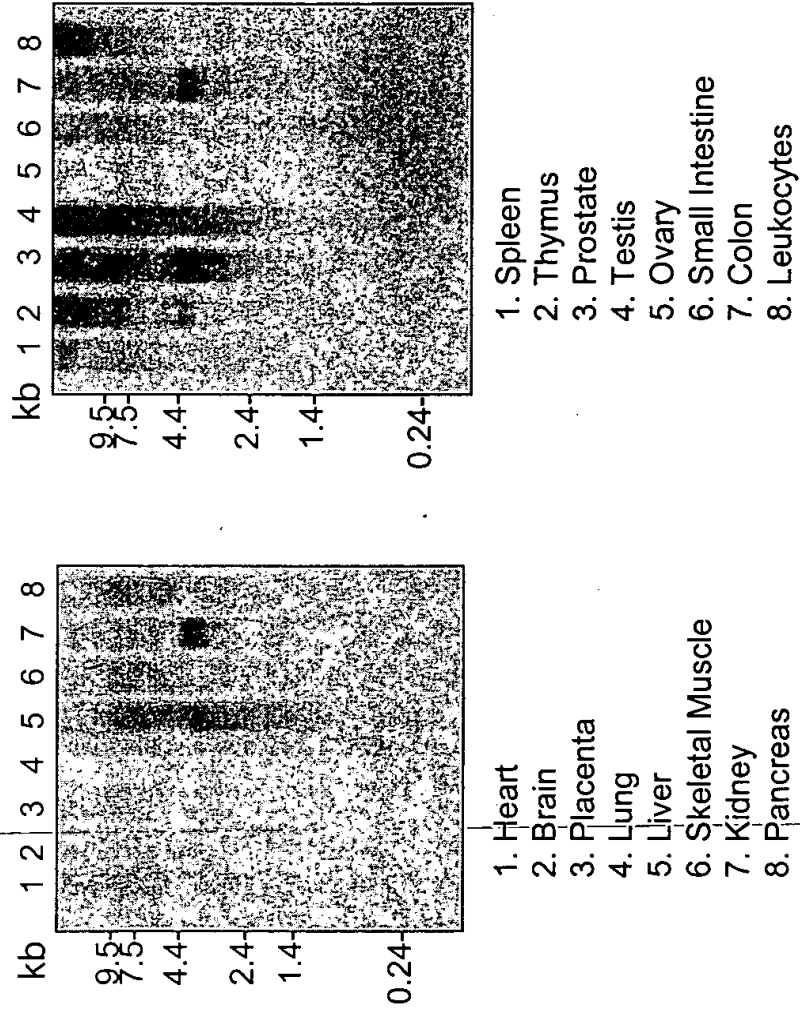


Figure 12: Expression of 161P2F10B in Patient Kidney Cancer Specimens and in Normal Tissues

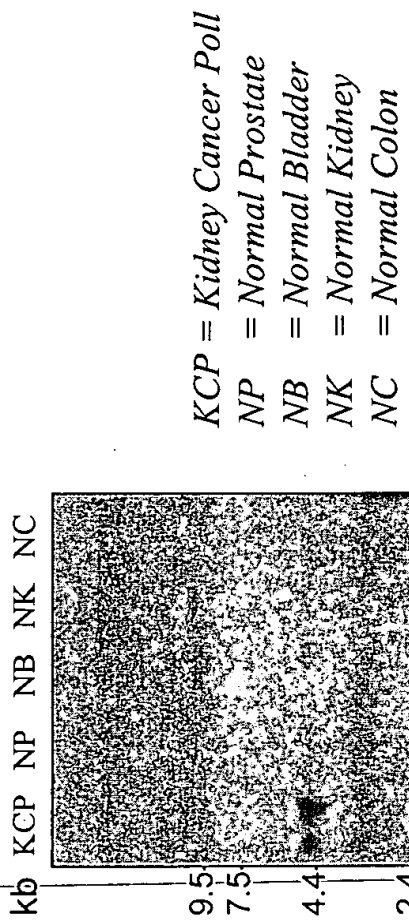
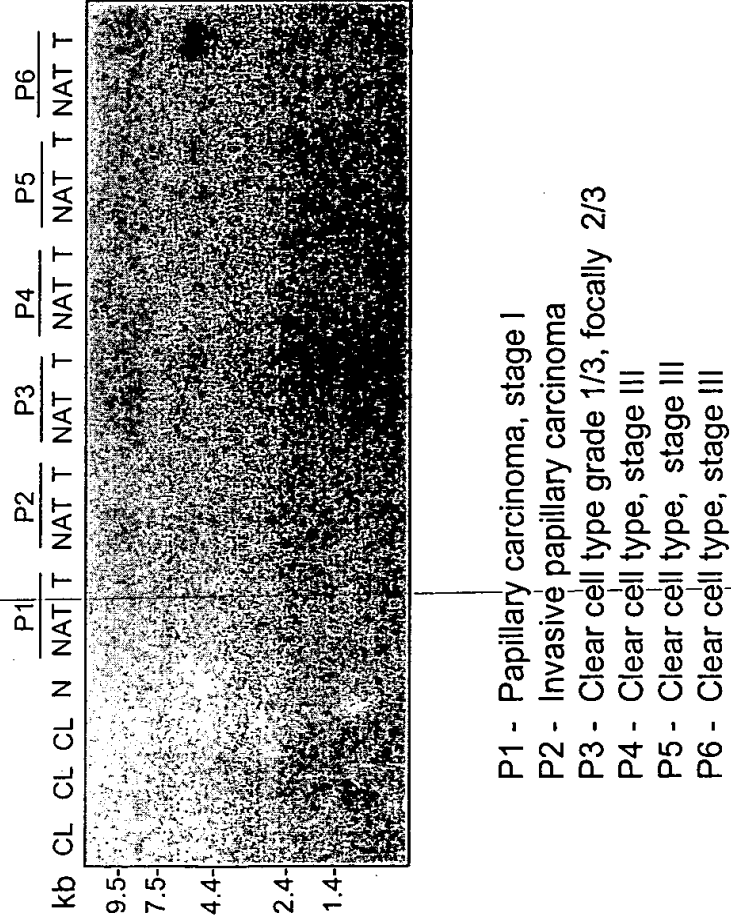
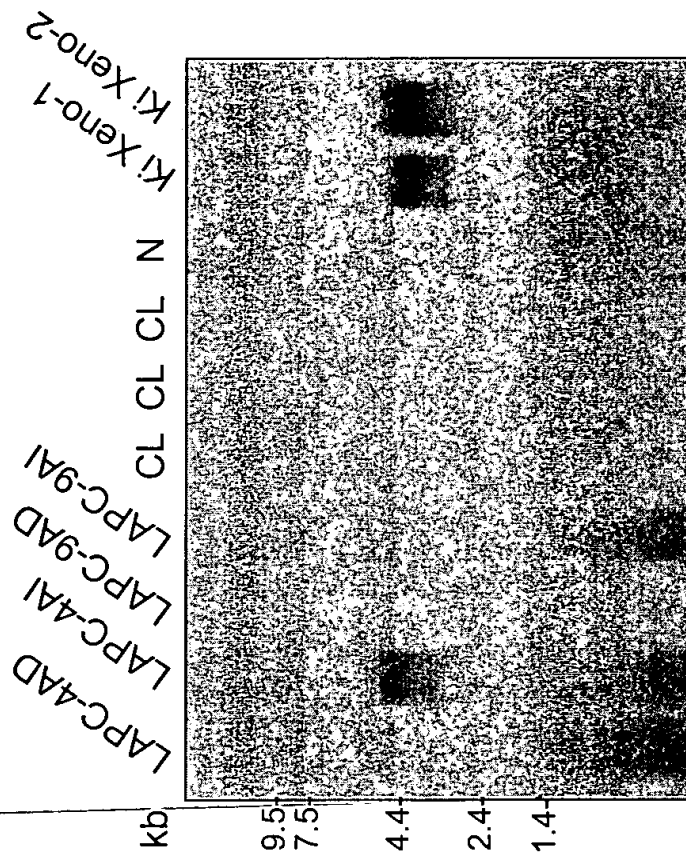


Figure 13: Expression of 161P2F10B in Kidney Cancer Patient Specimens



CL = cell lines listed in order: 769-P,
 A498, SW839
 N = Normal kidney
 NAT = Normal adjacent tumor
 T = Tumor
 P = Patient

Figure 14: Expression of 161P2F10B in Kidney Cancer Xenografts



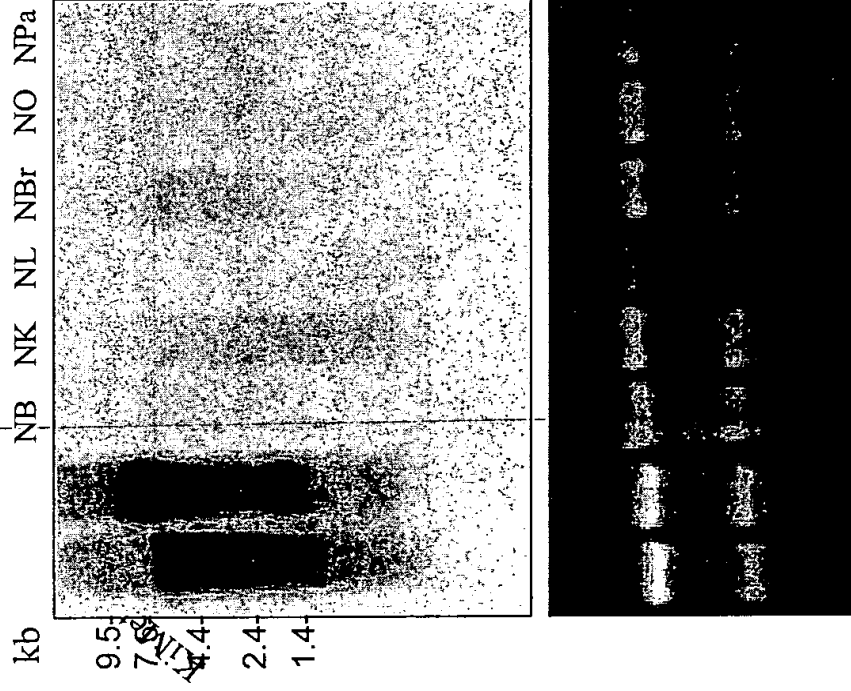
CL = cell lines listed in order: 769-P,

A498, Caki-1

N = Normal kidney

Ki Xeno = Kidney xenograft

Figure 15: Expression of 161P2F10B in Kidney Cancer Metastasis Specimens and in Normal Tissues



KiMet 1 = Kidney Metastasis to lung
KiMet 2 = Kidney Metastasis to lymph node
NB = Normal Bladder
NK = Normal Kidney
NL = Normal Lung
NBr = Normal Breast
NO = Normal Ovary
NPa = Normal Pancreas

Figure 16: Expression of 161P2F10B Protein by Immunohistochemistry in Kidney Cancer Patient Specimens

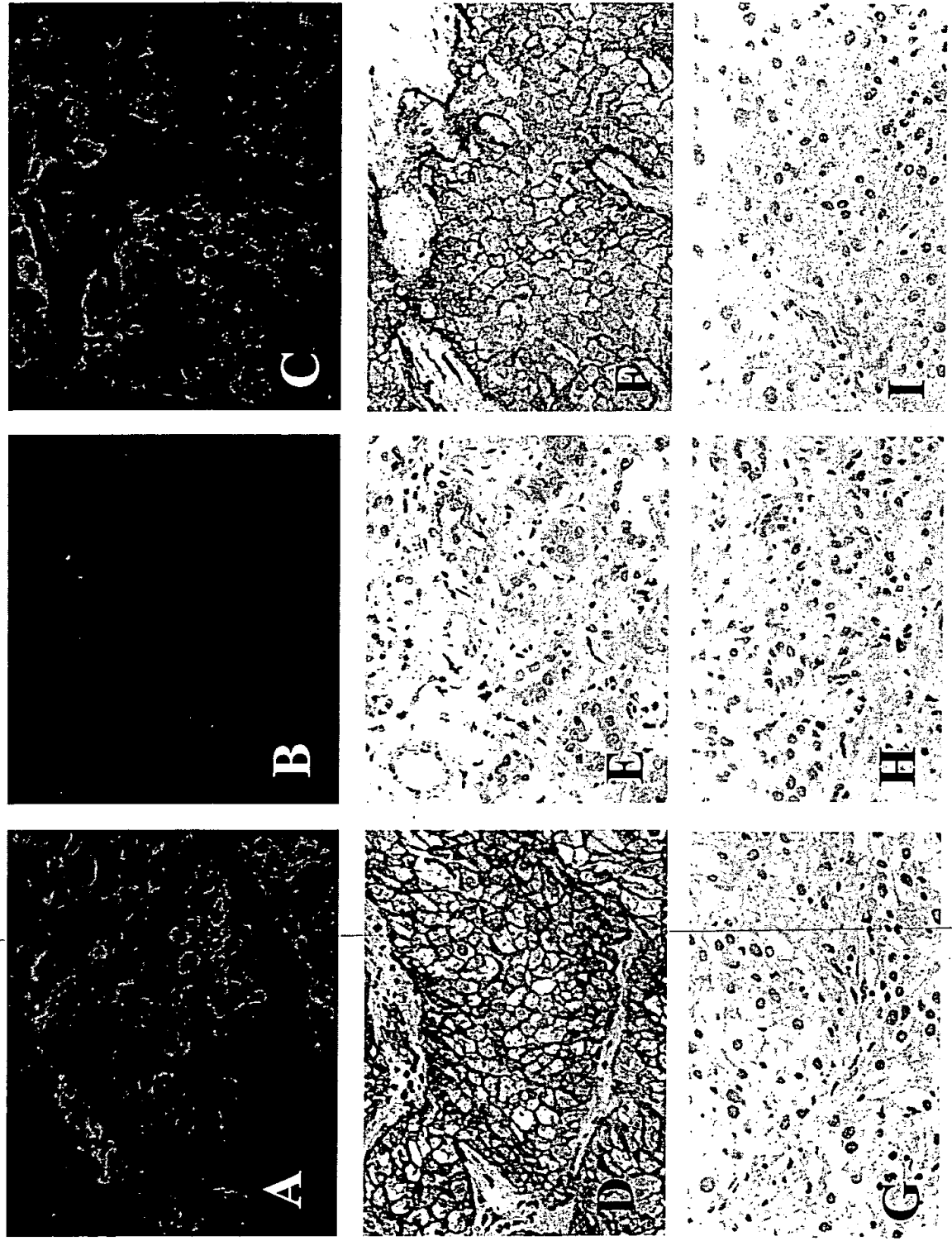
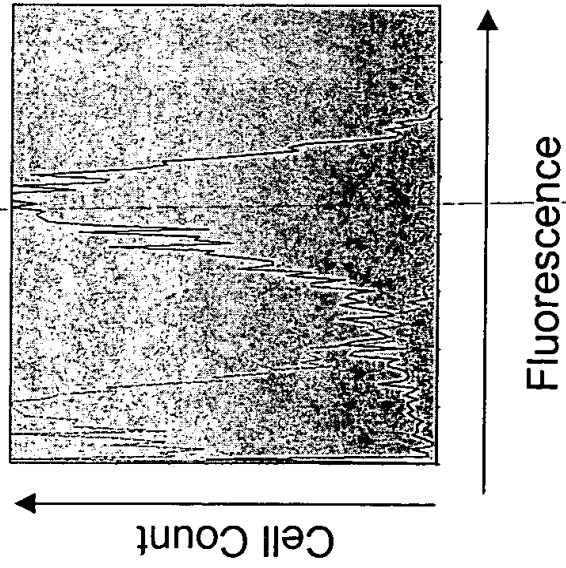
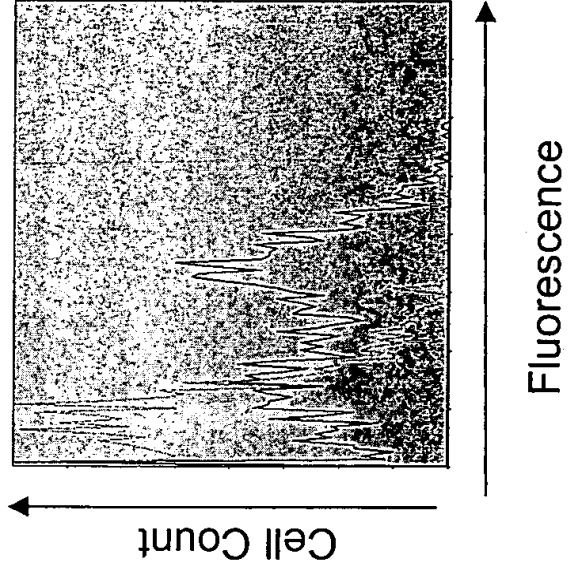


Figure 17: Expression of 161P2F10B Protein on the Cell Surface of Renal Cell Carcinoma Xenografts

A. Clear Cell Carcinoma



B. Renal Cancer Metastasis to LN



**Figure 18: Expression of 161P2F10B Protein by
Immunohistochemistry in Human Cancer Xenograft Tissues**

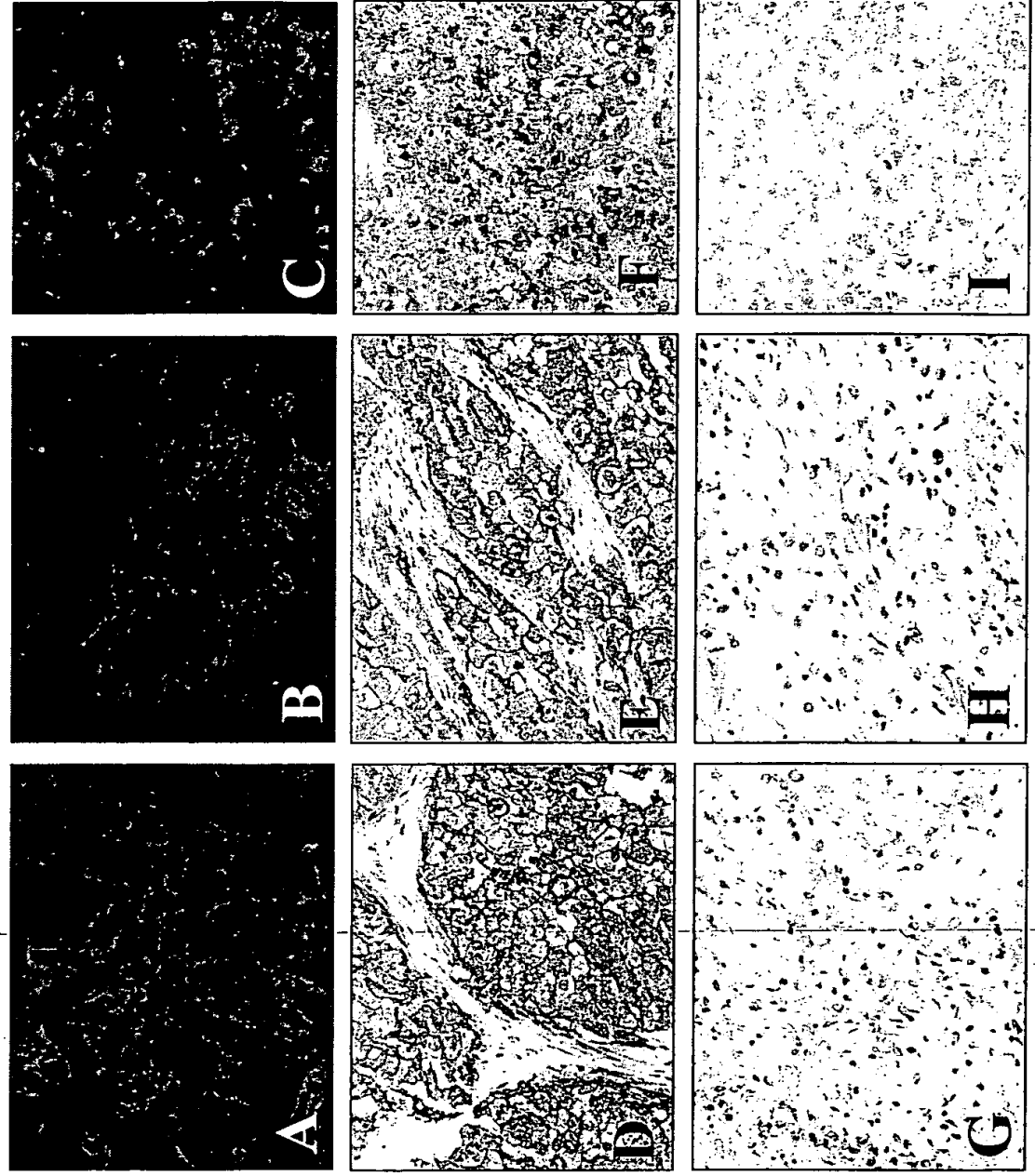


Figure 19A (Seq. ID. No. 751)

10 20 30 40 50 60 70
| | | | | | |
MESTLTLATEQPVKNTLKKYKIACIVLLALLVIMSLGLGLGLRLKLEKQGSCRKKCFDASFRGLENCR
ccccccccccccccccchhhhhhhhhhhhhhhhhhhhhchhhhhhhhhhhccccccccccccccccchcccc
CDVACKDRGDCCWDFEDTCVESTRIWMCNKFRCGETRLEASLCSCSDDCLQKDCADYKSVCQGETSWL
ccccccccccccccccccccchhhhhehhhhhccccccccceechccccccccccccccccccccccccch
EENCDDTAQQSQCPGFDLPPVILFSDMGFRAEYLYTWDTLMPNINKLKTGIIHISKYMRAMYPTKTFPNHY
ccccccccccccccccccccceeeccccchhhhhhhhhhhhhchhhhccccchhhhhecccccccccccc
TIVTGLYPESHGIIIDNNMYDVNLNKNFSLSSKEQNNPAWWHGQPMWLTAMYQGLKAATYFWPGSEVAING
eeeeccccccccchccccccccccccceccccccccccccccccchhhhhhhhhcccccccccccccccc
SFPSIYMPYNGSVPFEEERISTLLKWLDPKAERPRFYTMYPFEEPDSSGHAGGPVSARVIKALQVVDHAFG
ccccccccccccccccchhhhhhhhhhhhhccccccccccccccccccccccccccccchhhhhhhhhhhhhhh
MLMEGLKQRNLHNCVNIILLADHGMDQTYCNKMEYMTDYFPRINFFYMYEGPAPRIRAHNI PHDFFSFNS
hhhhhhhhhhccccccccccccccccccccchhhhhhhhhccccccccccccccccccccccccchhhcch
EEIVRNLSRKPDPQHFKPYLTPDLPKRLHYAKNVRIDKVHLFVDQQLAVRSKSNNTNCGGGNHGYNNEFR
hhhhhhhhccccccccccccccccccccchhhhhhhccccchhhhhhhhhhhheccccccccccccccccchhh
SMEAIFLAHGSPFKEKTEVEPFENIEVYNLMCDLLRIQPAPNNGTHGSLNHLLKVPFYEP SHAEEVSKFS
hhhhhhhhccccccccccccccccccccchhhhhhhhhhhhhccccccccccccccccchheccccccccccccchce
VCGFANPLPTESLDCFCPHLQNSTQLEQVNQMLNLTQEEITATVKVNLFPGRPRVLQKNVDHCLLYHREY
ccccccccccccccccchhhccccccccchhhhhhhhhhhchhhhhhhheccccccccccccccccccccchhh
VSGFGKAMRMPMWSSYTVPQLGDTSPPTVPDCLRADVRVPPSESQKCSFYLAADKNITHGFLYPPASNR
hhcc
TSDSQYDALITSNLVPMYEEFRKMWDYFHSVLLIKHATERNGVNVVSGPIFDYNYDGHFDAPDEITKHLA
ccchhhhhhhhhccccchhhhhhhhhhhhhhhhhhhhehhccccccccccccccccccccccccchhhhhhhhhcc
NTDVPIPTHYFVVLTSCKNKSHTPENC PGWLDVLPFIIPHRPTNVE SCPEGKPEALWVEERFTHAIARVR
cc
DVELLTGLDFYQDKVQPVSEILQLKTYLPTFETTI
hhehccccccchcchhchhhhhhehhhhcccccccc

c: random coil (31.31%)
e: extended strand (11.31%)
h: alpha helix (57.37%)

Figure 19B

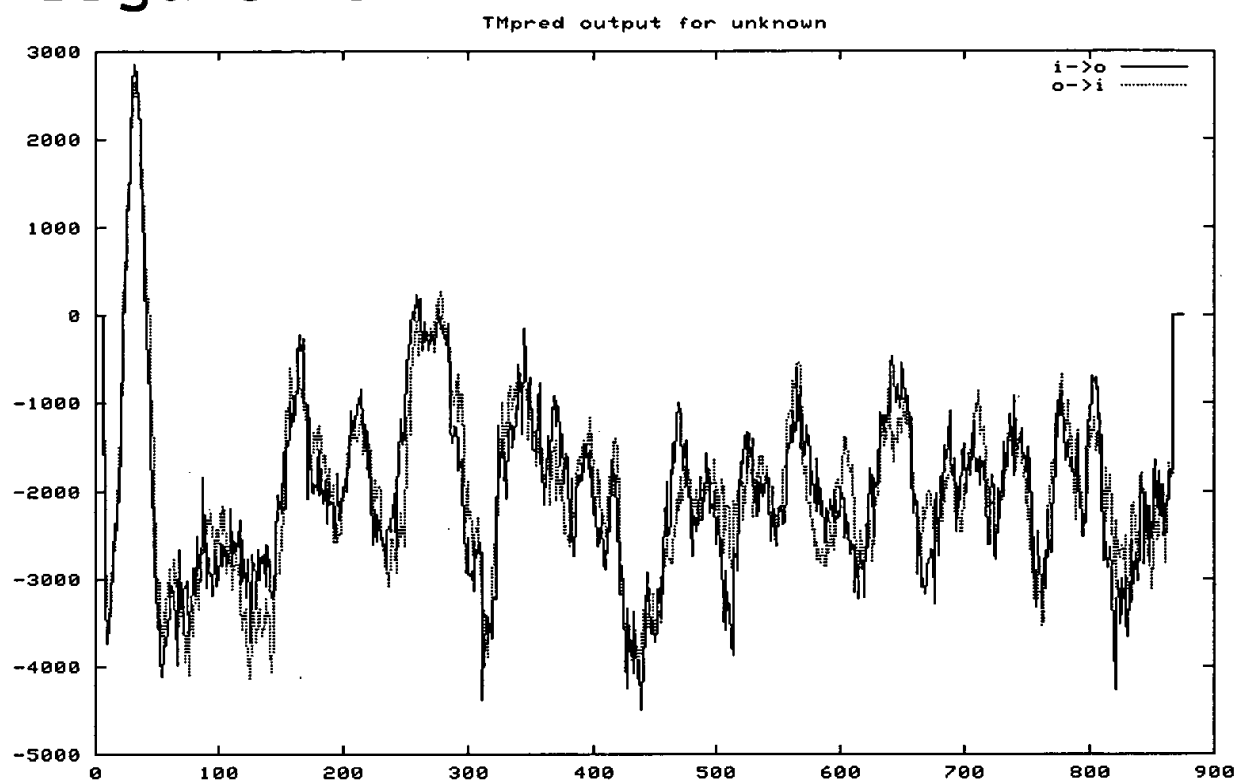
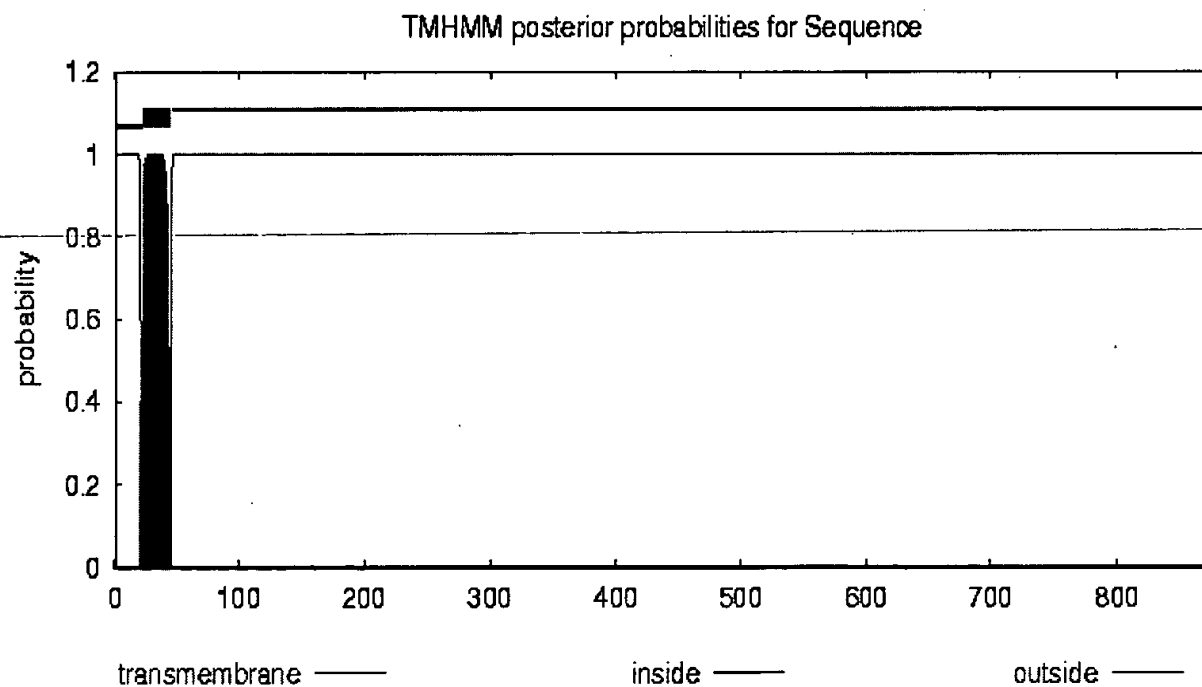


Figure 19C



**Figure 20 Expression of 161P2F10B in Human Patient Cancers
by Western Blot**

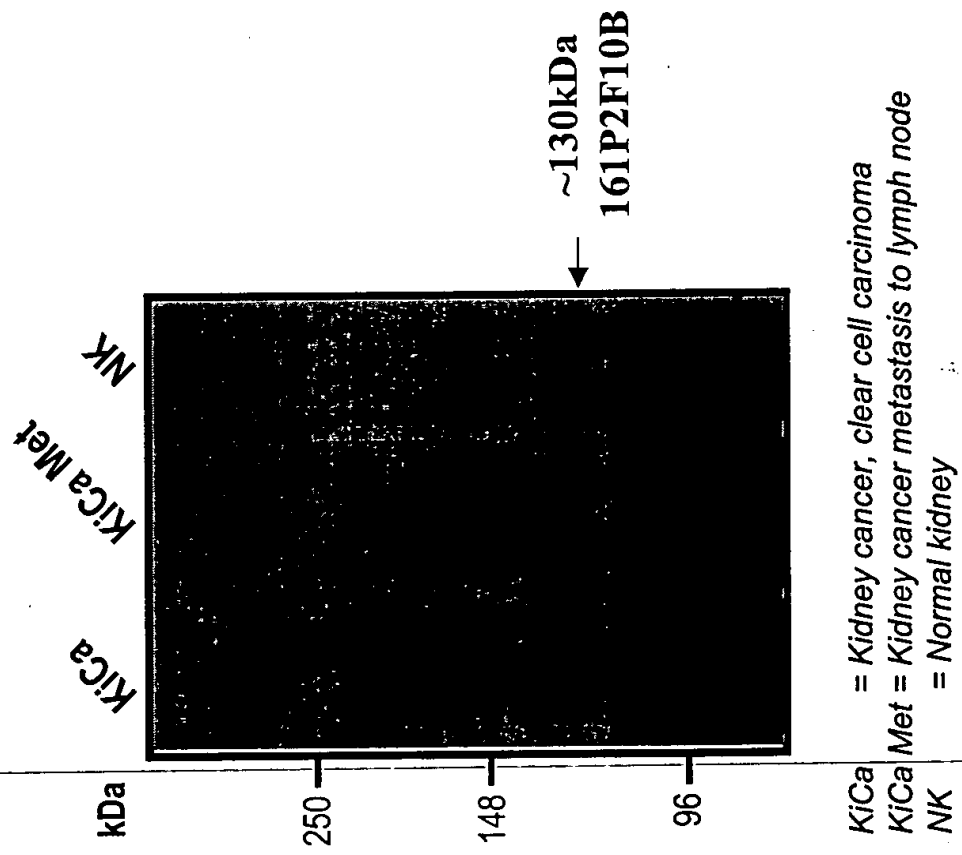
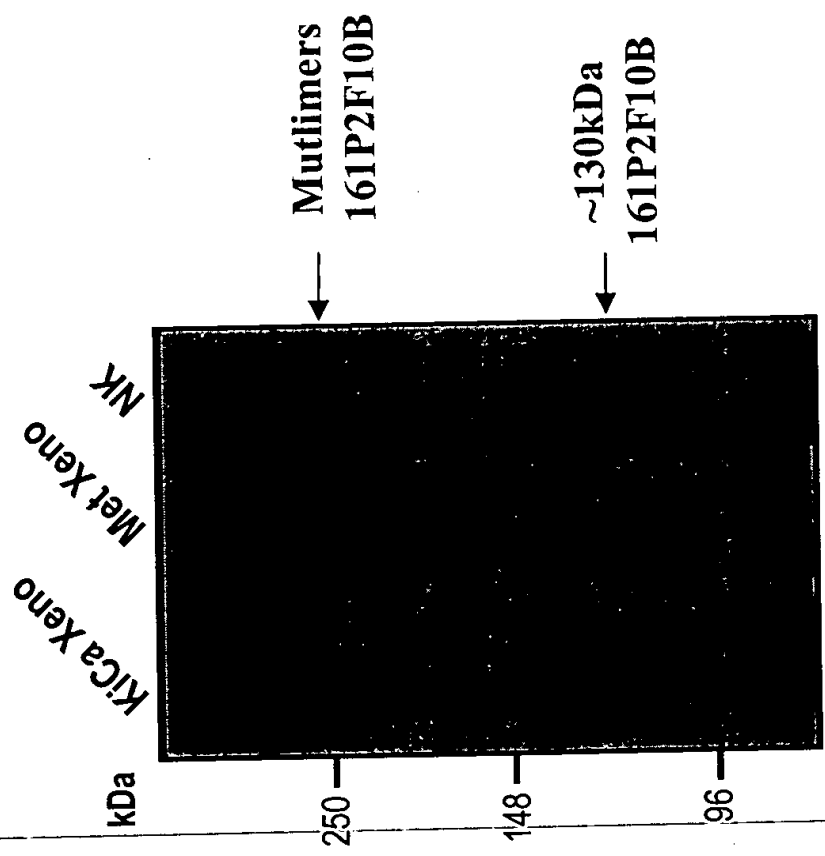


Figure 21 Expression of 161P2F10B in Human Xenograft
Tissues by Western Blot



KiCa Xeno = Xenograft of kidney cancer, clear cell carcinoma
Met Xeno = Xenograft from Kidney cancer metastasis to lymph node
NK = Normal kidney